CLAIMS

1. A method for the identification of one or more oligonucleotides on a microarray derived from a first species which can be used to analyse a corresponding nucleotide sequence from a second species or a distinct variety of the first species, the method comprising applying genomic DNA from the second species, or distinct variety of the first species, to the microarray derived from the first species and identifying/selecting oligonucleotides on the microarray which hybridise to the genomic DNA.

2. A method according to claim 1 wherein the identified oligonucleotides are used to analyse gene expression and/or gene transcripts in a second species or a distinct variety of the first species.

3. A method according to claim 1 wherein the identified oligonucleotides are used to identify nucleotide sequences which have been deleted from the second species or distinct variety of the first species.

4. A method according to claim 1 wherein the identified oligonucleotides are used to compare two or more varieties of the second species, or two or more distinct varieties of the first species.

5. A method according to any preceding claim wherein the identified oligonucleotides are used to analyse any form of nucleic acid or nucleic acid derivative, including mRNA, cRNA or cDNA, from the second species, or the distinct variety of the first species.

6. A method according to any preceding claim wherein the microarray comprises a number of probe sets, each probe set being specific to a gene transcript from the species from which the array is derived.

7. A method according to claim 7 wherein each probe set comprises between about 11 and about 20 probes which bind at various positions on the gene transcript.

8. A method according to claim 6 or 7 wherein the probe set comprises one or more probe pairs, in which each probe pair comprises a perfect match (PM) and a mismatch (MM) oligonucleotide probe.

9 A method according to any preceding claims wherein the oligonucleotides/probes are from about 15 to about 80 nucleotides in length.

10. A method according to claim 9 wherein the oligonucleotides/probes are from about 20 to about 30 nucleotides in length.

11. A method according to any preceding claim which includes the step of generating a mask defining only those probes which hybridised to the applied genomic DNA.

12. A method according to any of claims 1 to 10 in which the oligonucleotides which do not bind to the genomic DNA are selected.

13. A method according to any preceding claim which uses more than one microarray each from a different species.

14. A method of analysing nucleic acids from a second species, or a distinct variety of the a first species, using a microarray derived from a first species comprising:

applying genomic DNA of the second species, or the distinct variety of the first species, to the microarray derived from the first species;

identifying probes/oligonucleotides on the microarray to which the genomic DNA has hybridised;

selecting the probes/oligonucleotides on the microarray to which the genomic DNA has hybridised for use in further analysis;

applying mRNA, cDNA or cRNA from a tissue of the second species, or distinct variety of the first species, to a microarray derived from the first species;

analysing the pattern of hybridisation of the mRNA, cDNA or cRNA to the selected probes/oligonucleotides.

15. A method according to claim 14 in which the genomic DNA, mRNA, cDNA and/or cRNA is labelled before use.

16. The use of one or more oligonucleotides selected according to the method of any preceding claim to study gene expression in a second species, or a distinct variety of the first species.

17. The use of one or more oligonucleotides selected according to the method of any of claims 1 to 15 to identify a series of homologous genes to a first species on a large cloned fragment of genome from a second species using a vector associated construct.

18. The use of one or more oligonucleotides selected according to the method of any of claims 1 to 15 to study changes in gene structure

between a first species and a second species, or a distinct variety of the first species.

19. The use of claim 18 wherein the changes include deletions, insertions and/or mutations.

20. The use of one or more oligonucleotides selected according to the method of any of claims 1 to 15 as primers for amplification.

21. A kit for selecting oligonucleotides on a microarray comprising a microarray derived from a first species and instructions to use the method of the invention with genomic DNA of a second species or a distinct variety of the first species.

22. A kit for analysing gene expression in a second species or a distinct variety of a first species comprising a microarray derived from a first species and instructions to use the microarray according to the method of the invention.

23. A computer system for selecting oligonucleotide probes comprising:

a co-ordinate extraction means arranged to extract the co-ordinates of probes on a microarray derived from a first species to which genomic DNA from a second species, or a distinct variety of the first species, has been applied which display a hybridisation intensity with the genomic DNA that is above background to generate a match co-ordinate output;

a mismatch elimination means arranged to identify and eliminate mismatch probes with a higher hybridisation intensity than perfect match

probes from the match co-ordinate output to generate a perfect match co-ordinate output;

a chip description file (CDF) generation means arranged to compare the first species CDF with the perfect match co-ordinate output and to generate a further CDF comprising the co-ordinates present in both the first species CDF and the perfect match output.

24. A computer system according to claim 23 comprising a background determination means.

25. A computer system for generating a mask comprising:
a reader arranged to detect where genomic DNA has hybridised to a probe on a microarray and to produce data indicative of where hybridisation has occurred; and
a processor arranged to combine the data from the reader with a CDF for the microarray to produce a mask.

26. A computer system according to claim 25 wherein the genomic DNA hybridised to the microarray probes is from a species or variety different to that used to make the microarray.

27. A computer system according to claim 25 or 26 wherein the data generated by the reader is a set of co-ordinates corresponding to the probes which have hybridised to the genomic DNA.

28. A computer system according to any of claims 25, 26 or 27 wherein the mask is a computer programme arranged to operate a reader so that when the mask is applied the reader only considers specific coordinates on a microarray.

29. Use of a mask generated by the computer system of any of claims 25 to 28 to tailor a microarray from a first species to a different species, or distinct variant of the first species.

30. A method of making a mask comprising the steps of:
applying genomic DNA from a second species or a distinct variety of a first species to a microarray derived from a first species;
analysing with a reader the microarray to determine which probes are hybridised to the genomic DNA;
comparing the CDF file for the microarray with the data from the reader;
generating a mask which represents the coordinates of probes on the microarray which hybridised to the genomic DNA.

31. A method according to claim 30 wherein at least one of the steps of making a mask is undertaken on a computer.

32. A data carrier carrying data arranged to control a computer system to carry out the method of making a mask according to claim 30 or 31 or to operate as a computer system according to any of claims 23 to 28.